

WO 2005/051999

1/7

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb

<130> 30287P-EP

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> Human

<400> 1

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1 5 10 15Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
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35 40 45His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2

<211> 172

<212> PRT

<213> Human

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val

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1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asp Ser Gly
50 55 60Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3

<211> 13

<212> PRT

<213> Human

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<210> 4

<211> 312

<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)..(312)

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1 5 10 15gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

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tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc	144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile	
35 40 45	
tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc	192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly	
50 55 60	
agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct	240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser	
65 70 75 80	
gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac	288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr	
85 90 95	
acg ttc gga ggg ggg acc aag ctg	312
Thr Phe Gly Gly Thr Lys Leu	
100	

<210> 5
<211> 104
<212> PRT
<213> hybridoma

<400> 5	
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Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile	
35 40 45	
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly	
50 55 60	
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser	
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Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr	
85 90 95	
Thr Phe Gly Gly Thr Lys Leu	
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<210> 6
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<212> DNA
<213> hybridoma

<220>
<221> CDS
<222> (1)...(312)

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1 5 10 15	

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat	96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr	
20	25
	30
ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga	144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly	
35	40
	45
tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag	192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys	
50	55
	60
gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg	240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met	
65	70
	75
	80
ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat	288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr	
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	95
ggt ccg ttt gct tac tgg ggc caa	312
Gly Pro Phe Ala Tyr Trp Gly Gln	
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<210> 7
<211> 104
<212> PRT
<213> hybridoma

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	30
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly	
35	40
	45
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys	
50	55
	60
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met	
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85	90
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Gly Pro Phe Ala Tyr Trp Gly Gln	
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<212> DNA
<213> hybridoma

<220>
<221> CDS
<222> (1)...(330)

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 cag agg gcc acc atc tca tac agg gcc agc aaa agt gtc agt aca tct 96
 Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
 20 25 30
 ggc tat agt tat atg cac tgg aac caa cag aaa cca gga cag cca ccc 144
 Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 aga ctc ctc atc tat ctt gta tcc aac cta gaa tct ggg gtc cct gcc 192
 Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60
 agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat 240
 Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 cct gtg gag gag gag gat gct gca acc tat tac tgt cag cac att agg 288
 Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
 85 90 95
 gag ctt aca cgt tcg gag ggg gga cca agc tgg aga tct aac a 331
 Glu Leu Thr Arg Ser Glu Gly Pro Ser Trp Arg Ser Asn
 100 105 110

<210> 9
<211> 110
<212> PRT
<213> hybridoma

<400> 9
 Arg Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Gln Arg Ala Thr Ile Ser Tyr Arg Ala Ser Lys Ser Val Ser Thr Ser
 20 25 30
 Gly Tyr Ser Tyr Met His Trp Asn Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45
 Arg Leu Leu Ile Tyr Leu Val Ser Asn Leu Glu Ser Gly Val Pro Ala
 50 55 60
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80
 Pro Val Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ile Arg
 85 90 95
 Glu Leu Thr Arg Ser Glu Gly Pro Ser Trp Arg Ser Asn
 100 105 110

<210> 10
<211> 343
<212> DNA

<213> hybridoma

<220>

<221> CDS

<222> (1)..(342)

<400> 10

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Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser	
1	5
	10
	15

ctg tcc atc aca tgc acc gtc tca ggg ttc tca act agc tat ggt	96
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr Gly	
20	25
	30

gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gta	144
Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val	
35	40
	45

gtg ata tgg agt gat gga agc aca acc tat aat tca gct ctc aaa tcc	192
Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser	
50	55
	60

aga ctg agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa	240
Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys	
65	70
	75
	80

atg aac agt ctccaa act gat gac aca gcc atg tac tac tgt gcc aga	288
Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg	
85	90
	95

gag cct ccc acg acg tac gtt tgc tta ctg ggg cca agg gac cac tct	336
Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser	
100	105
	110

aga tta a	343
Arg Leu	

<210> 11

<211> 114

<212> PRT

<213> hybridoma

<400> 11

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	15

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20	25
	30

Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Val	
35	40
	45

Val Ile Trp Ser Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser	
50	55
	60

Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys	
65	70
	75
	80

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg	
85	90
	95

Glu Pro Pro Thr Thr Tyr Val Cys Leu Leu Gly Pro Arg Asp His Ser
100 105 110

Arg Leu

10/580813

AP9 Rec'd PCT/PTO 25 MAY 2006

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450

<141> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver: 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

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Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
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20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIb

<400> 2
Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3
<211> 13
<212> PRT
<213> human

<220>
<223> glycopeptide CDE [126-137]

<400> 3
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<210> 4
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable light region of mAb GB3

<220>
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comprised by an antibody

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1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

acg ttc gga ggg ggg acc aag ctg 312
Thr Phe Gly Gly Thr Lys Leu
100

<210> 5
<211> 104
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

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1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Thr Lys Leu
100

<210> 6
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable heavy region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

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Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met				
65	70	75	80	
ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat				288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr				
85	90	95		
ggt ccg ttt gct tac tgg ggc caa				312
Gly Pro Phe Ala Tyr Trp Gly Gln				
100				
<210> 7				
<211> 104				
<212> PRT				
<213> Unknown Organism				
<223> Description of Unknown Organism: sequence				
comprised by an antibody				
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Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr				
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Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly				
35	40	45		
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys				
50	55	60		
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met				
65	70	75	80	
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr				
85	90	95		
Gly Pro Phe Ala Tyr Trp Gly Gln				
100				

<210> 8				
<211> 309				
<212> DNA				
<213> Unknown Organism				
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<221> CDS				
<222> (1)..(309)				
<223> variable light region of mAb CE5				
<220>				
<223> Description of Unknown Organism: sequence				
comprised by an antibody				

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 1 5 10 15

 gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca 96
 Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
 20 25 30

 tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat 144
 Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
 35 40 45

 aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga 192
 Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

 tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat 240
 Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

 ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cg^g acg ttc 288
 Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
 85 90 95

 ggt gga ggg acc aag ctc gag 309
 Gly Gly Gly Thr Lys Leu Glu
 100

<210> 9
 <211> 103
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 9
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 1 5 10 15

 Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
 20 25 30

 Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
 35 40 45

 Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

 Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

 Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
 85 90 95

 Gly Gly Gly Thr Lys Leu Glu

100

<210> 10
<211> 339
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (3)..(338)
<223> variable heavy region of mAb CES

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

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Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
1 5 10 15

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
20 25 30

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
35 40 45

tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg 191
Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
50 55 60

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac 239
Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
65 70 75

agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga 287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg
80 85 90 95

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
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tca g 339
Ser

<210> 11
<211> 112
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
1 5 10 15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
20 25 30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
35 40 45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
50 55 60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
65 70 75 80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
85 90 95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110

10/580813

IAP9 Recupt/PTO 25 MAY 2006

30287PW1.txt
SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissenschaften
<120> Substance binding human IgG Fc receptor IIb (Fc gamma RIIB)

<130> 30287P_WO HC

<140> PCT/EP2004/013450
<141> 2004-11-26

<150> EP03027000.3
<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIIa

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Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
1 5 10 15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95
Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125
Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

30287PW1.txt

<210> 2

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIB

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3

<211> 13

<212> PRT

<213> human

<220>

<223> glycopeptide CDE [126-137]

<400> 3

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
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<210> 4

<211> 312

<212> DNA

<213> Unknown Organism

30287PW1.txt

<220>

<221> CDS

<222> (1)..(312)

<223> variable light region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

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aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga	48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly	
1 5 10 15	

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac	96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr	
20 25 30	

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc	144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile	
35 40 45	

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc	192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly	
50 55 60	

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct	240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser	
65 70 75 80	

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac	288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr	
85 90 95	

acg ttc gga ggg ggg acc aag ctg	312
Thr Phe Gly Gly Thr Lys Leu	
100	

<210> 5

<211> 104

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly	
1 5 10 15	

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr	
20 25 30	

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile	
35 40 45	

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly	
50 55 60	

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser	
65 70 75 80	

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr	
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85

30287Pw1.txt
90

95

Thr Phe Gly Gly Thr Lys Leu
100

<210> 6
<211> 312
<212> DNA
<213> Unknown Organism

<220>
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<222> (1)..(312)
<223> variable heavy region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

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<400> 6
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Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 . 5 10 15

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gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
 20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
 Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac	aag	gcc	aca	ctt	act	ata	gat	aga	tcc	tcc	agc	aca	gcc	tac	atg	240
Asp	Lys	Ala	Thr	Leu	Thr	Ile	Asp	Arg	Ser	Ser	Ser	Thr	Ala	Tyr	Met	
65			70						75					80		

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
 Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
 85 90 95

ggt ccg ttt gct tac tgg ggc caa
Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 7
<211> 104
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 7
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

30287PW1.txt

20

25

30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
 35 40 45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
 50 55 60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
 65 70 75 80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
 85 90 95

Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 8

<211> 309

<212> DNA

<213> Unknown Organism

<220>

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<222> (1)..(309)

<223> variable light region of mAb CE5

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

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gag ctc acc cag tct cca gcc tcc ctt tct gcg tct gtg gga gaa act	48
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr	
1 5 10 15	

gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca	96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala	
20 25 30	

tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat	144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr	
35 40 45	

aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga	192
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	

tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat	240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp	
65 70 75 80	

ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cggt acg ttc	288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe	
85 90 95	

ggt gga ggg acc aag ctc gag	309
Gly Gly Gly Thr Lys Leu Glu	
100	

30287PW1.txt

<210> 9
 <211> 103
 <212> PRT
 <213> Unknown Organism
 <223> Description of Unknown Organism: sequence
 comprised by an antibody

<400> 9
 Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
 20 25 30

Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
 35 40 45

Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
 85 90 95

Gly Gly Gly Thr Lys Leu Glu
 100

<210> 10
 <211> 339
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (3)..(338)
 <223> variable heavy region of mAb CE5

<220>
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 comprised by an antibody

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 tg cag gag tca gga cct ggc ctg gtg gcg ccc tca cag agc ctg tcc 47
 Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
 1 5 10 15

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
 Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
 20 25 30

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
 Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
 35 40 45

tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg 191
 Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
 50 55 60

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac 239

30287PW1.txt

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn	65	70	75	
agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga				287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg	80	85	90	95
gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc				335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser	100	105	110	
tca g				339
Ser				

<210> 11

<211> 112

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile	1	5	10	15
---	---	---	----	----

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp	20	25	30	
---	----	----	----	--

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp	35	40	45	
---	----	----	----	--

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser	50	55	60	
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Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser	65	70	75	80
---	----	----	----	----

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp	85	90	95	
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Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	100	105	110	
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10/580813 11. März 2005
IAP9 Rec'd PCT/PTO 25 MAY 2006

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Förderung der Wissenschaften

<120> Substance binding human IgG Fc receptor IIb (Fc gamma RIIb)

<130> 30287P_WO HC

<140> PCT/EP2004/013450

<141> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

<400> 1

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
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20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIb

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125

His	Ser	Gly	Asp	Tyr	His	Cys	Thr	Gly	Asn	Ile	Gly	Tyr	Thr	Leu	Tyr
145					150					155					160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3
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<213> human

<220>
<223> glycopeptide CDE [126-137]

<400> 3
Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
1 5 10

<210> 4
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable light region of mAb GB3

<220>
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comprised by an antibody

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aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cg^g gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc			144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile			
35	40	45	
tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc			192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly			
50	55	60	
agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct			240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser			
65	70	75	80
gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac			288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr			
85	90	95	
acg ttc gga ggg ggg acc aag ctg			312
Thr Phe Gly Gly Thr Lys Leu			
100			

<210> 5

<211> 104

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly			
1	5	10	15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr			
20	25	30	

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile			
35	40	45	

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly			
50	55	60	

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser			
65	70	75	80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr			
85	90	95	

Thr Phe Gly Gly Thr Lys Leu

<210> 6
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable heavy region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 6
gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 48
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Thr Ala Tyr Met
65 70 75 80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95

ggt ccg ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 7
<211> 104
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 7

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95

Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 8
<211> 309
<212> DNA
<213> Unknown Organism

<220>

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<222> (1)..(309)

<223> variable light region of mAb CE5

<220>

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comprised by an antibody

<400> 8

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Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr

1	5	10	15	
gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca				96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala				
20	25	30		
tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat				144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr				
35	40	45		
aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga				192
Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly				
50	55	60		
tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat				240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp				
65	70	75	80	
ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc				288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe				
85	90	95		
ggt gga ggg acc aag ctc gag				309
Gly Gly Gly Thr Lys Leu Glu				
100				

<210> 9
<211> 103
<212> PRT
<213> Unknown Organism
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 9				
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr				
1	5	10	15	
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala				
20	25	30		
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr				
35	40	45		
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly				
50	55	60		
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp				

65 70 75 80

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Leu Glu
100

<210> 10

<211> 339

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (3)..(338)

<223> variable heavy region of mAb CES

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

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Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
1 5 10 15

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
20 25 30

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
35 40 45

tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg 191
Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
50 55 60

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac 239
Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
65 70 75

agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga 287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg
80 85 90 95

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
100 105 110

tca g 339
Ser

<210> 11

<211> 112

<212> PRT

<213> Unknown Organism

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
1 5 10 15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
20 25 30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
35 40 45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
50 55 60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
65 70 75 80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
85 90 95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110